

2113#5



OIPE

RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/965,536A

TIME: 12:48:41

Input Set : A:\30534118.app

Output Set: N:\CRF3\02212002\I965536A.raw

p.5

3 <110> APPLICANT: FEDER, J. N.
 4 MINTIER, G.
 5 RAMANATHAN, C. S.
 6 HAWKEN, D. R.
 8 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,
 9 EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
 11 <130> FILE REFERENCE: DOO41NP
 13 <140> CURRENT APPLICATION NUMBER: 09/965,536A
 14 <141> CURRENT FILING DATE: 2001-09-26
 16 <150> PRIOR APPLICATION NUMBER: 60/235,713
 17 <151> PRIOR FILING DATE: 2000-09-27
 19 <150> PRIOR APPLICATION NUMBER: 60/261,781
 20 <151> PRIOR FILING DATE: 2001-01-16
 22 <150> PRIOR APPLICATION NUMBER: 60/306,605
 23 <151> PRIOR FILING DATE: 2001-07-19
 25 <150> PRIOR APPLICATION NUMBER: 60/310,436
 26 <151> PRIOR FILING DATE: 2001-08-03
 28 <160> NUMBER OF SEQ ID NOS: 61
 30 <170> SOFTWARE: PatentIn Ver. 2.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2214
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
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 40 tgcttacccc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180
 41 gagaactgtg gtgacactag tggatgggag accatatattg gcacagtgc tggaaatgct 240
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 46 aggaaagcat tttttggatt atgtaatctg caaatattat atctcaacca caactgcatt 540
 47 acaacctca gacctggaat attcaaagac ttacatcagc taacttggt aattctagat 600
 48 gacaatccaa taaccagaat ttcacagcgc ttgtttacgg gattaaattc cttgtttttc 660
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59 ggcattgagat ctttcattaa agctgaaaat acaactcacg ctatgtccat caaaatcctt 1320
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68 aaaaccgcct tgcagaccac agaagtaagg aattgttttg gaagagagg gtgtgttgca 1860
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80 <213> ORGANISM: Homo sapiens

82 <400> SEQUENCE: 2

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87             20             25             30
89 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
90             35             40             45
92 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
93             50             55             60
95 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
96 65             70             75             80
98 Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
99             85             90             95
101 Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
102             100            105            110
104 Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
105             115            120            125
107 Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
108             130            135            140
110 Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
111 145            150            155            160
113 Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn
114             165            170            175
116 His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His
117             180            185            190
119 Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser
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125 Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro
126 225                      230                      235                      240
128 Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr
129      245                      250                      255
131 Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
132      260                      265                      270
134 Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
135      275                      280                      285
137 Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser
138      290                      295                      300
140 Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser
141 305                      310                      315                      320
143 Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys
144      325                      330                      335
146 Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
147      340                      345                      350
149 Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
150      355                      360                      365
152 Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
153      370                      375                      380
155 Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
156 385                      390                      395                      400
158 Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
159      405                      410                      415
161 Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
162      420                      425                      430
164 His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
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167 Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
168      450                      455                      460
170 Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu
171 465                      470                      475                      480
173 Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu
174      485                      490                      495
176 Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
177      500                      505                      510
179 Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
180      515                      520                      525
182 Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp
183      530                      535                      540
185 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
186 545                      550                      555                      560
188 Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
189      565                      570                      575
191 Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
192      580                      585                      590
194 Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu

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200 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val
201 625          630          635          640
203 Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
204          645          650          655
206 Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
207          660          665          670
209 Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
210          675          680          685
212 Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
213 690          695          700
215 Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
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242 cagcagaatg gctcctgtca ctgcattcca atggcagctg tactatctac caaccgtgct 180
243 gaggacagca ccaaagggtt ctctcctcac ccacatgcc tgaaaagcac atgtgaattc 240
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251 tttttctgaa ggttgcccag ggcacaaaca aattggacac tttcactgct aaaaagtaca 720
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253 ctttcataaa atatgcagat aagaagtgtt aaatgggatt caagaattat ggttttattt 840
254 gggactgttt gcatactcac aatggttttg ttctcattgt ttttaacaaa aaagcaatga 900
255 agtttggggt ggttttttga aaacgaaact gaaaaaaatt atatgtgaaa atgagaactg 960
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257 aaaaag
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261 <211> LENGTH: 2142

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RAW SEQUENCE LISTING

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Input Set : A:\30534118.app

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262 <212> TYPE: DNA

263 <213> ORGANISM: Homo sapiens

265 <400> SEQUENCE: 5

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268 tgcttaccoc gagcttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180
269 gagaactgtg gtgacactag tggatgggcg accatatttg gcacagtga tggaaatgct 240
270 aacagcgtgg ccttaacaca ggagtgtctt ctaaaacagt atccacaatg ctgtgactgc 300
271 aaagaaactg aattggaatg tgtaaatggg gacttaaagt ctgtgccgat gattttctaac 360
272 aatgtgacat taactgtctt taagaaaaac aaaatccaca gtcttcaga taaagttttc 420
273 atcaaataca caaaacttaa aaagatattt cttcagcata attgcattag acacatatcc 480
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307 <213> ORGANISM: Homo sapiens

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313 Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr
314           20           25           30
316 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys

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Use of n and/or Xaa has been detected in the Sequence Listing.
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 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
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